

SEQUENCE LISTING

<110> McCarthy, Sean A.

<120> NOVEL CRSP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
THEREFOR

<130> MEI-008

<140> 09/009,802

<141> 1998-01-20

<150> 08/842,898

<151> 1997-04-17

<150> 60/071,589

<151> 1998-01-15

<160> 19

<170> PatentIn Ver. 2.0

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (38)..(1087)

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<223> 'n' at position 1146 may be any nucleotide

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acc ctg ctg tgc ctg ctg ctg gcg gcg gcg gtc ccc acg gcc ccc gcg 103
Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala Val Pro Thr Ala Pro Ala
10 15 20

ccc gct ccg acg gcg acc tcg gct cca gtc aag ccc ggc ccg gct ctc 151
Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu
25 30 35

agc tac ccg cag gag gag gcc acc ctc aat gag atg ttc cgc gag gtt 199
Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val
40 45 50

gag gaa ctg atg gag gac acg cag cac aaa ttg cgc agc gcg gtg gaa 247
Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu
55 60 65 70

gag atg gag gca gaa gaa gct gct gct aaa gca tca tca gaa gtg aac	295
Glu Met Glu Ala Glu Glu Ala Ala Lys Ala Ser Ser Glu Val Asn	
75 80 85	
ctg gca aac tta cct ccc agc tat cac aat gag acc aac aca gac acg	343
Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr	
90 95 100	
aac gtt gga aat aat acc atc cat gtg cac cga gaa att cac aag ata	391
Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile	
105 110 115	
acc aac aac cag act gga caa atg gtc ttt tca gag aca gtt atc aca	439
Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr	
120 125 130	
tct gtg gga gac gaa gaa ggc aga agg agc cac gag tgc atc atc gac	487
Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp	
135 140 145 150	
gag gac tgt ggg ccc agc atg tac tgc cag ttt gcc agc ttc cag tac	535
Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr	
155 160 165	
acc tgc cag cca tgc cgg ggc cag agg atg ctc tgc acc cgg gac agt	583
Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser	
170 175 180	
gag tgc tgt gga gac cag ctg tgt gtc tgg ggt cac tgc acc aaa atg	631
Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met	
185 190 195	
gcc acc agg ggc agc aat ggg acc atc tgt gac aac cag agg gac tgc	679
Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys	
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cag ccg ggg ctg tgc tgt gcc ttc cag aga ggc ctg ctg ttc cct gtg	727
Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val	
215 220 225 230	
tgc aca ccc ctg ccc gtg gag ggc gag ctt tgc cat gac ccc gcc agc	775
Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser	
235 240 245	
cgg ctt ctg gac ctc atc acc tgg gag cta gag cct gat gga gcc ttg	823
Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu	
250 255 260	
gac cga tgc cct tgt gcc agt ggc ctc ctc tgc cag ccc cac agc cac	871
Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His	
265 270 275	
agc ctg gtg tat gtg tgc aag ccg acc ttc gtg ggg agc cgt gac caa	919
Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln	
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Cmt.

gat ggg gag atc ctg ctg ccc aga gag gtc ccc gat gag tat gaa gtt 967
 Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val
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ggc agc ttc atg gag gag gtg cgc cag gag ctg gag gac ctg gag agg 1015
 Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg
 315 320 325

agc ctg act gaa gag atg gcg ctg agg gag cct gcg gct gcc gcc gct 1063
 Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala Ala
 330 335 340

gca ctg ctg gga agg gaa gag att tagatctgga ccaggctgtg ggtagatgtg 1117
 Ala Leu Leu Gly Arg Glu Glu Ile
 345 350

caatagaaat agctaattta tttccccang tgtgtgcttt aagcgtgggc tgaccaggct 1177

tcttctaca tcttcttccc agtaagtttc cctcttggtc tgacagcatg aggtgttgtg 1237

catttggtca gctccccag gctgttctcc aggcttcaca gtctggtgct tgggagagtc 1297

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ccactacccc acaccagcct tggtgccacc aaaagtgtc cccaaaagga aggagaaatgg 1897

gatttttctt ttgaggcatg cacatctgga attaaggtca aactaattct cacatccctc 1957

taaaagtaaa ctactgttag gaacagcagt gttctcacag tgtggggcag cgtccttct 2017

aatgaagaca atgatattga cactgtccct ctttggcagt tgcattagta actttgaaag 2077

gtatatgact gagcgtagca tacagggtta cctgcagaaa cagtacttag gtaattgtag 2137

ggcgaggatt ataaatgaaa tttgcaaaat cacttagcag caactgaaga caattatcaa 2197

ccacgtggag aaaatcaaac cgagcagggc tgtgtgaaac atggttgtaa tatgcgactg 2257

cgaacactga actctacgcc actccacaaa tgatgttttc aggtgtcatg gactgttgcc 2317

B¹
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accatgtatt catccagagt tcttaaagtt taaagttgca catgattgta taagcatgct 2377
ttcttttgagt tttaaattat gtataaacat aagttgcatt tagaaatcaa gcataaatca 2437
cttcaactgc taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2479

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<212> PRT
<213> Homo sapiens

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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80
Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
85 90 95
Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
100 105 110
Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
115 120 125
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
130 135 140
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145 150 155 160
Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
165 170 175
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
180 185 190
Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
195 200 205
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220

B!
cont.

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
 225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
 245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
 275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
 290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
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1				5					10					15		
gtc	ccc	acg	gcc	ccc	gcg	ccc	gct	ccg	acg	gcg	acc	tgc	gct	cca	gtc	96
Val	Pro	Thr	Ala	Pro	Ala	Pro	Ala	Pro	Thr	Ala	Thr	Ser	Ala	Pro	Val	
			20						25				30			
aag	ccc	ggc	ccg	gct	ctc	agc	tac	ccg	cag	gag	gag	gcc	acc	ctc	aat	144
Lys	Pro	Gly	Pro	Ala	Leu	Ser	Tyr	Pro	Gln	Glu	Glu	Ala	Thr	Leu	Asn	
		35					40					45				
gag	atg	ttc	cgc	gag	gtt	gag	gaa	ctg	atg	gag	gac	acg	cag	cac	aaa	192
Glu	Met	Phe	Arg	Glu	Val	Glu	Glu	Leu	Met	Glu	Asp	Thr	Gln	His	Lys	
	50					55					60					
ttg	cgc	agc	gcg	gtg	gaa	gag	atg	gag	gca	gaa	gaa	gct	gct	gct	aaa	240
Leu	Arg	Ser	Ala	Val	Glu	Glu	Met	Glu	Ala	Glu	Glu	Ala	Ala	Ala	Lys	
65					70				75						80	

B1
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gca tca tca gaa gtg aac ctg gca aac tta cct ccc agc tat cac aat	288
Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn	
85 90 95	
gag acc aac aca gac acg aac gtt gga aat aat acc atc cat gtg cac	336
Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His	
100 105 110	
cga gaa att cac aag ata acc aac aac cag act gga caa atg gtc ttt	384
Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe	
115 120 125	
tca gag aca gtt atc aca tct gtg gga gac gaa gaa ggc aga agg agc	432
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser	
130 135 140	
cac gag tgc atc atc gac gag gac tgt ggg ccc agc atg tac tgc cag	480
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln	
145 150 155 160	
ttt gcc agc ttc cag tac acc tgc cag cca tgc cgg ggc cag agg atg	528
Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met	
165 170 175	
ctc tgc acc cgg gac agt gag tgc tgt gga gac cag ctg tgt gtc tgg	576
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp	
180 185 190	
ggt cac tgc acc aaa atg gcc acc agg ggc agc aat ggg acc atc tgt	624
Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys	
195 200 205	
gac aac cag agg gac tgc cag ccg ggg ctg tgc tgt gcc ttc cag aga	672
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg	
210 215 220	
ggc ctg ctg ttc cct gtg tgc aca ccc ctg ccc gtg gag ggc gag ctt	720
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu	
225 230 235 240	
tgc cat gac ccc gcc agc cgg ctt ctg gac ctc atc acc tgg gag cta	768
Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu	
245 250 255	
gag cct gat gga gcc ttg gac cga tgc cct tgt gcc agt ggc ctc ctc	816
Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu	
260 265 270	
tgc cag ccc cac agc cac agc ctg gtg tat gtg tgc aag ccg acc ttc	864
Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe	
275 280 285	
gtg ggg agc cgt gac caa gat ggg gag atc ctg ctg ccc aga gag gtc	912
Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val	
290 295 300	

B1
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ccc gat gag tat gaa gtt ggc agc ttc atg gag gag gtg cgc cag gag   960
Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
305                      310                      315                      320

ctg gag gac ctg gag agg agc ctg act gaa gag atg gcg ctg agg gag   1008
Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
                      325                      330                      335

cct gcg gct gcc gcc gct gca ctg ctg gga agg gaa gag att           1050
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aagg atg gtg gcg gcc gtc ctg ctg ggg ctg agc tgg ctc tgc tct ccc   169
      Met Val Ala Ala Val Leu Leu Gly Leu Ser Trp Leu Cys Ser Pro
        1                      5                      10                      15

ctg gga gct ctg gtc ctg gac ttc aac aac atc agg agc tct gct gac   217
Leu Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp
                      20                      25                      30

ctg cat ggg gcc cgg aag ggc tca cag tgc ctg tct gac acg gac tgc   265
Leu His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys
                      35                      40                      45

aat acc aga aag ttc tgc ctc cag ccc cgc gat gag aag ccg ttc tgt   313
Asn Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys
                      50                      55                      60

gct aca tgt cgt ggg ttg cgg agg agg tgc cag cga gat gcc atg tgc   361
Ala Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys
                      65                      70                      75

tgc cct ggg aca ctc tgt gtg aac gat gtt tgt act acg atg gaa gat   409
Cys Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp
      80                      85                      90                      95

gca acc cca ata tta gaa agg cag ctt gat gag caa gat ggc aca cat   457
Ala Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His
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B1
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Lys Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu
130 135 140

agt tgt ctg aga act ttt gac tgt ggc cct gga ctt tgc tgt gct cgt 601
Ser Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg
145 150 155

cat ttt tgg acg aaa att tgt aag cca gtc ctt ttg gag gga cag gtc 649
His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val
160 165 170 175

tgc tcc aga aga ggg cat aaa gac act gct caa gct cca gaa atc ttc 697
Cys Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe
180 185 190

cag cgt tgc gac tgt ggc cct gga cta ctg tgt cga agc caa ttg acc 745
Gln Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr
195 200 205

agc aat cgg cag cat gct cga tta aga gta tgc caa aaa ata gaa aag 793
Ser Asn Arg Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys
210 215 220

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Leu

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His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn
35 40 45

Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala
50 55 60

Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys Cys
65 70 75 80

Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala
85 90 95

B1
Cont.

Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala
100 105 110

Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys
115 120 125

Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser
130 135 140

Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
145 150 155 160

Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys
165 170 175

Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln
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<222> (1)..(672)

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Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp Leu
20 25 30

cat ggg gcc cgg aag ggc tca cag tgc ctg tct gac acg gac tgc aat 144
His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn
35 40 45

acc aga aag ttc tgc ctc cag ccc cgc gat gag aag ccg ttc tgt gct 192
Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala
50 55 60

aca tgt cgt ggg ttg cgg agg agg tgc cag cga gat gcc atg tgc tgc 240
Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys Cys
65 70 75 80

B1
Cont.

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Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala	
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acc cca ata tta gaa agg cag ctt gat gag caa gat ggc aca cat gca	336
Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala	
100 105 110	
gaa gga aca act ggg cac cca gtc cag gaa aac caa ccc aaa agg aag	384
Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys	
115 120 125	
cca agt att aag aaa tca caa ggc agg aag gga caa gag gga gaa agt	432
Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser	
130 135 140	
tgt ctg aga act ttt gac tgt ggc cct gga ctt tgc tgt gct cgt cat	480
Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His	
145 150 155 160	
ttt tgg acg aaa att tgt aag cca gtc ctt ttg gag gga cag gtc tgc	528
Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys	
165 170 175	
tcc aga aga ggg cat aaa gac act gct caa gct cca gaa atc ttc cag	576
Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln	
180 185 190	
cgt tgc gac tgt ggc cct gga cta ctg tgt cga agc caa ttg acc agc	624
Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr Ser	
195 200 205	
aat cgg cag cat gct cga tta aga gta tgc caa aaa ata gaa aag cta	672
Asn Arg Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys Leu	
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B1
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	Met Met Ala Leu Gly Ala Ala	
	1 5	
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Gly Ala Thr Arg Val Phe Val Ala Met Val Ala Ala Ala Leu Gly Gly		
10 15 20		
cac cct ctg ctg gga gtg agc gcc acc ttg aac tcg gtt ctc aat tcc	209	
His Pro Leu Leu Gly Val Ser Ala Thr Leu Asn Ser Val Leu Asn Ser		
25 30 35		
aac gct atc aag aac ctg ccc cca ccg ctg ggc ggc gct gcg ggg cac	257	
Asn Ala Ile Lys Asn Leu Pro Pro Pro Leu Gly Gly Ala Ala Gly His		
40 45 50 55		
cca ggc tct gca gtc agc gcc gcg ccg gga atc ctg tac ccg ggc ggc	305	
Pro Gly Ser Ala Val Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly		
60 65 70		
aat aag tac cag acc att gac aac tac cag ccg tac ccg tgc gca gag	353	
Asn Lys Tyr Gln Thr Ile Asp Asn Tyr Gln Pro Tyr Pro Cys Ala Glu		
75 80 85		
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Gly Asp Ala Gly Val Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys		
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Arg Cys Met Arg His Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn		
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Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg Gly Glu Ile Glu		
140 145 150		
gaa acc atc act gaa agc ttt ggt aat gat cat agc acc ttg gat ggc	593	
Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser Thr Leu Asp Gly		
155 160 165		
tat tcc aga aga acc acc ttg tct tca aaa atg tat cac acc aaa gga	641	
Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr His Thr Lys Gly		
170 175 180		
caa gaa ggt tct gtt tgt ctc cgg tca tca gac tgt gcc tca gga ttg	689	
Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys Ala Ser Gly Leu		
185 190 195		
tgt tgt gct aga cac ttc tgg tcc aag atc tgt aaa cct gtc ctg aaa	737	
Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys Lys Pro Val Leu Lys		
200 205 210 215		

B1
Cont

gaa ggt caa gtg tgt acc aag cat agg aga aaa ggc tct cat gga cta 785
 Glu Gly Gln Val Cys Thr Lys His Arg Arg Lys Gly Ser His Gly Leu
 220 225 230

gaa ata ttc cag cgt tgt tac tgt gga gaa ggt ctg tct tgc cgg ata 833
 Glu Ile Phe Gln Arg Cys Tyr Cys Gly Glu Gly Leu Ser Cys Arg Ile
 235 240 245

cag aaa gat cac cat caa gcc agt aat tct tct agg ctt cac act tgt 881
 Gln Lys Asp His His Gln Ala Ser Asn Ser Ser Arg Leu His Thr Cys
 250 255 260

cag aga cac taaaccagct atccaaaatg cagtgaactc cttttatata 930
 Gln Arg His
 265

atagatgcta tgaaaacctt ttatgacctt catcaactca atcctaagga tatacaagtt 990
 ctgtgggtttc agttaagcat tccaataaca ccttccaaaa acctggagtg taagagcttt 1050
 gtttctttat ggaactcccc tgtgattgca gtaaattact gtattgtaaa ttctcagtgt 1110
 ggcacttacc tgtaaagca atgaaacttt taattatttt tctaaagggtg ctgcactgcc 1170
 tatttttcct cttgttatgt aaatttttgt acacattgat tgttatcttg actgacaaat 1230
 attctatatt gaactgaagt aaatcatttc agcttatagt tcttaaaagc ataacccttt 1290
 accccatttn attctagagt cnagaacgca aggatctctt ggaatgacaa atgataggta 1350
 cctaaaatgt aacatgaaaa tactagctta ttttctgaaa tgtactatct taatgcttaa 1410
 attatatttc cctttaggct gtgatagttt ttgaaataaa atttaacatt taatatcatg 1470
 aaatgktata agtagacata aaaaaaaaaa aaaaaaaaaa agggcggccg ctagactag 1529

<210> 8
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met
 1 5 10 15
 Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr
 20 25 30
 Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro
 35 40 45
 Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro
 50 55 60

B1
 Cont.

Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr
 65 70 75 80
 Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr
 85 90 95
 Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu
 100 105 110
 Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys
 115 120 125
 Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn
 130 135 140
 His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn
 145 150 155 160
 Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser
 165 170 175
 Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser
 180 185 190
 Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys
 195 200 205
 Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg
 210 215 220
 Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly
 225 230 235 240
 Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn
 245 250 255
 Ser Ser Arg Leu His Thr Cys Gln Arg His
 260 265

<210> 9
 <211> 798
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(798)

<400> 9
 atg atg gct ctg ggc gca gcg gga gct acc cgg gtc ttt gtc gcg atg 48
 Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met
 1 5 10 15

B1
cont

gta gcg gcg gct ctc ggc ggc cac cct ctg ctg gga gtg agc gcc acc Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr 20 25 30	96
ttg aac tcg gtt ctc aat tcc aac gct atc aag aac ctg ccc cca ccg Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro 35 40 45	144
ctg ggc ggc gct gcg ggg cac cca ggc tct gca gtc agc gcc gcg ccg Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro 50 55 60	192
gga atc ctg tac ccg ggc ggg aat aag tac cag acc att gac aac tac Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr 65 70 75 80	240
cag ccg tac ccg tgc gca gag gac gag gag tgc ggc act gat gag tac Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr 85 90 95	288
tgc gct agt ccc acc cgc gga ggg gac gca ggc gtg caa atc tgt ctc Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu 100 105 110	336
gcc tgc agg aag cgc cga aaa cgc tgc atg cgt cac gct atg tgc tgc Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys 115 120 125	384
ccc ggg aat tac tgc aaa aat gga ata tgc gtg tct tct gat caa aat Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn 130 135 140	432
cat ttc cga gga gaa att gag gaa acc atc act gaa agc ttt ggt aat His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn 145 150 155 160	480
gat cat agc acc ttg gat ggg tat tcc aga aga acc acc ttg tct tca Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser 165 170 175	528
aaa atg tat cac acc aaa gga caa gaa ggt tct gtt tgt ctc cgg tca Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser 180 185 190	576
tca gac tgt gcc tca gga ttg tgt tgt gct aga cac ttc tgg tcc aag Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys 195 200 205	624
atc tgt aaa cct gtc ctg aaa gaa ggt caa gtg tgt acc aag cat agg Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg 210 215 220	672
aga aaa ggc tct cat gga cta gaa ata ttc cag cgt tgt tac tgt gga Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly 225 230 235 240	720

B1
Cont.

gaa ggt ctg tct tgc cgg ata cag aaa gat cac cat caa gcc agt aat 768
Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn
245 250 255

tct tct agg ctt cac act tgt cag aga cac 798
Ser Ser Arg Leu His Thr Cys Gln Arg His
260 265

<210> 10
<211> 702
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(537)

<400> 10
gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga 48
Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
1 5 10 15

tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga 96
Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
20 25 30

gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc 144
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
35 40 45

cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt 192
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
50 55 60

act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg 240
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
65 70 75 80

gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa 288
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
85 90 95

ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg 336
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
100 105 110

ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc 384
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
115 120 125

cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg 432
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
130 135 140

B1
Cont

ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa 480
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
145 150 155 160

gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt 528
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
165 170 175

cag aaa att tgatcaccat tgaggaacat catcaattgc agactgtgaa 577
Gln Lys Ile

gttgtgtatt taatgcatta tagcatggtg gaaaataagg ttcagatgca gaagaatggc 637

taaaataaga aacgtgataa gaatatagat gatcacaaaa aaaaaaaaaa aaaagatgcg 697

gccgc 702

<210> 11

<211> 179

<212> PRT

<213> Homo sapiens

<400> 11

Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
1 5 10 15

Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
20 25 30

Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
35 40 45

Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
50 55 60

Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
65 70 75 80

Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
85 90 95

Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
100 105 110

Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
115 120 125

His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
130 135 140

Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
145 150 155 160

Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
165 170 175

B!
Ant

Gln Lys Ile

<210> 12
<211> 537
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(537)

<400> 12
gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga 48
Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
1 5 10 15
tca tgc gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga 96
Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
20 25 30
gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc 144
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
35 40 45
cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt 192
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
50 55 60
act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg 240
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
65 70 75 80
gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa 288
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
85 90 95
ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg 336
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
100 105 110
ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc 384
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
115 120 125
cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg 432
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
130 135 140
ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa 480
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
145 150 155 160

B1
cont

gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt 528
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
165 170 175

cag aaa att 537
Gln Lys Ile

<210> 13
<211> 928
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (75)..(800)

<400> 13
ctcgaggcca aaattcggca cgaggccggg ctgtggtcta gcataaaggc ggagcccaga 60

agaaggggcg ggggt atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg 110
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg
1 5 10

cat ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc 158
His Leu Leu Val Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser
15 20 25

gct gca gct cct atc cat gat gct gac gcc caa gag agc tcc ttg ggt 206
Ala Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly
30 35 40

ctc aca ggc ctc cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg 254
Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu
45 50 55 60

aaa ggt aac ctg ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg 302
Lys Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met
65 70 75

gac ttc cgg ggc ctc cct ggg aac tac cac aaa gag gag aac cag gag 350
Asp Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu
80 85 90

cac cag ctg ggg aac aac acc ctc tcc agc cac ctc cag atc gac aag 398
His Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys
95 100 105

atg acc gac aac aag aca gga gag gtg ctg atc tcc gag aat gtg gtg 446
Met Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val
110 115 120

gca tcc att caa cca gcg gag ggg agc ttc gag ggt gat ttg aag gta 494
Ala Ser Ile Gln Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val
125 130 135 140

B1
cont.

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ccc agg atg gag gag aag gag gcc ctg gta ccc atc cag aag gcc acg 542
Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr
               145                      150                      155

gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att 590
Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile
               160                      165                      170

aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac 638
Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His
               175                      180                      185

tgg ctc agc gag aag cga cac cgc ctg cag gcc atc cgg gat gga ctc 686
Trp Leu Ser Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu
               190                      195                      200

cgc aag ggg acc cac aag gac gtc cta gaa gag ggg acc gag agc tcc 734
Arg Lys Gly Thr His Lys Asp Val Leu Glu Gly Thr Glu Ser Ser
205                      210                      215                      220

tcc cac tcc agg ctg tcc ccc cga aag acc cac tta ctg tac atc ctc 782
Ser His Ser Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu
               225                      230                      235

agg ccc tct cgg cag ctg taggggtggg gaccggggag cacctgcctg 830
Arg Pro Ser Arg Gln Leu
               240

tagcccccat cagaccctgc cccaagcacc atatggaaat aaagttcttt cttacatcta 890

aaaaaaaaaa aaaaaaaaaa aaaaaaattg gcggccgc 928

```

<210> 14
 <211> 242
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
 1 5 10 15
 Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
 20 25 30
 Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
 35 40 45
 Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
 50 55 60
 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
 65 70 75 80
 Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
 85 90 95

B1
Cont.

Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
100 105 110

Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
115 120 125

Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
130 135 140

Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His
145 150 155 160

Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
165 170 175

Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu
180 185 190

Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
195 200 205

His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg
210 215 220

Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg
225 230 235 240

Gln Leu

<210> 15
<211> 726
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(726)

<400> 15
atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg cat ctg ctg gtc 48
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
1 5 10 15

ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc gct gca gct cct 96
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
20 25 30

atc cat gat gct gac gcc caa gag agc tcc ttg ggt ctc aca ggc ctc 144
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
35 40 45

B1
Cont.

cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg aaa ggt aac ctg Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu 50 55 60	192
ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg gac ttc cgg ggc Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly 65 70 75 80	240
ctc cct ggg aac tac cac aaa gag gag aac cag gag cac cag ctg ggg Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly 85 90 95	288
aac aac acc ctc tcc agc cac ctc cag atc gac aag atg acc gac aac Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn 100 105 110	336
aag aca gga gag gtg ctg atc tcc gag aat gtg gtg gca tcc att caa Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln 115 120 125	384
cca gcg gag ggg agc ttc gag ggt gat ttg aag gta ccc agg atg gag Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu 130 135 140	432
gag aag gag gcc ctg gta ccc atc cag aag gcc acg gac agc ttc cac Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His 145 150 155 160	480
aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att aag ctg cca cgg Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg 165 170 175	528
cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac tgg ctc agc gag Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu 180 185 190	576
aag cga cac cgc ctg cag gcc atc cgg gat gga ctc cgc aag ggg acc Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr 195 200 205	624
cac aag gac gtc cta gaa gag ggg acc gag agc tcc tcc cac tcc agg His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg 210 215 220	672
ctg tcc ccc cga aag acc cac tta ctg tac atc ctc agg ccc tct cgg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg 225 230 235 240	720
cag ctg Gln Leu	726

B1
Cont.

<210> 16
<211> 2381
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (110)..(1156)

<400> 16

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agctcagctt tggtcattcg aattgggcgg cggccagcgc ggaacaaac atg cag cgg 118
Met Gln Arg
1

ctc ggg ggt att ttg ctg tgt aca ctg ctg gcg gcg gcg gtc ccc act 166
Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala Val Pro Thr
5 10 15

gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg gag ccg ggc 214
Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala Glu Pro Gly
20 25 30 35

cca gct ctc aac tac cct cag gag gaa gct acg ctc aat gag atg ttt 262
Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe
40 45 50

cga gag gtg gag gag ctg atg gaa gac act cag cac aaa ctg cgc agt 310
Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser
55 60 65

gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa acg tcc tct 358
Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Thr Ser Ser
70 75 80

gag gtg aac ctg gca agc tta cct ccc aac tat cac aat gag acc agc 406
Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn Glu Thr Ser
85 90 95

acg gag acc agg gtg gga aat aac aca gtc cat gtg cac cag gaa gtt 454
Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His Gln Glu Val
100 105 110 115

cac aag ata acc aac aac cag agt gga cag gtg gtc ttt tct gag aca 502
His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe Ser Glu Thr
120 125 130

gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc cat gaa tgt 550
Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser His Glu Cys
135 140 145

atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag ttc tcc agc 598
Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln Phe Ser Ser
150 155 160

ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg cta tgc acc 646
Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met Leu Cys Thr
165 170 175

B!
Cont.

cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg ggt cac tgc	694
Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp Gly His Cys	
180 185 190 195	
acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt gac aac cag	742
Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys Asp Asn Gln	
200 205 210	
agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga ggc ctg ctg	790
Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu	
215 220 225	
ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc tgc cat gac	838
Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp	
230 235 240	
ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg gag cct gaa	886
Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Glu	
245 250 255	
gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta tgc cag cca	934
Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro	
260 265 270 275	
cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc gtg ggc agc	982
His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe Val Gly Ser	
280 285 290	
cat gac cac agt gag gag agc cag ctg ccc agg gag gcc ccg gat gag	1030
His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala Pro Asp Glu	
295 300 305	
tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag ctg gaa gac	1078
Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu Leu Glu Asp	
310 315 320	
ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg cct gcc cct	1126
Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly Pro Ala Pro	
325 330 335	
gtg gag tca cta ggc gga gag gag gag att taggccccaga cccagctgag	1176
Val Glu Ser Leu Gly Gly Glu Glu Glu Ile	
340 345	
tcactggtag atgtgcaata gaaatggcta atttattttc ccaggagtgt ccccaagtgt	1236
ggaatggccg cagctccttc ccagtagctt ttcctctggc ttgacaaggt acagtgcagt	1296
acatttcttc cagccgccct gcttctctga cttgggaaag acaggcatgg cgggtaaggg	1356
cagcggtgag tcgtccctcg ctgttgctag aaacgctgtc ttgttcttca tggatggaag	1416
atttgtttga agggagagga tgggaagggg tgaagtctgc tcatgatgga tttgggggat	1476
acagggagga ggatgcctgc cttgcagacg tggacttggc aaaatgtaac ctttgctttt	1536

B1
Cont.

gtcttgccgc gctcccatgg gctgaggcag tggctacaca agagctatgc tgctctgtgg 1596
cctcccacat attcatccct gtgtttcagc tcttacctca ctgtcagcac agcccttcat 1656
agccacgccc cctcttgctc accacagcct aggaggggac cagaggggac ttctctcaga 1716
gccccatgct ctctctctca accccatacc agcctctgtg ccagcgacag tctttccaaa 1776
tggagggagt gaaatccttt ggtttaatta ttttctcctt caaggcacgc ctgccactaa 1836
ggtcaggctg acttgcatgt cctctaacg ttctgtacag tgtggtggac actgtcttcc 1896
accgactgct tcaatacctc tgaaagccag tgctcggagt gcagttcgtg taaattaatt 1956
tgcaggaagt atacttggct aattgtaggg ctaggattgt gaatgaaatt tgcaaagtcg 2016
cttagcaaca atggaaagcc tttctcagtc acaccgagaa gtcacaacca agccagggtg 2076
tgtagagtac agctgtgaca tacagacaga agaaggctgg gctggatgtc aggcctcaga 2136
tgacggtttc aggtgccagg aactattacc attctgtatc tatccagagt tattaataatt 2196
gaaagttgca cacatttgta taagcatgcc tttctcctga gttttaaatt atatgtatac 2256
acaaacatgt ggccctcaaa gatcatgcac aaaccactac tctttgctaa ttcttgact 2316
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gccgc 2381

<210> 17
<211> 349
<212> PRT
<213> Homo sapiens

<400> 17
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Val Pro Thr Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala
20 25 30
Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80
Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
85 90 95

B1
Cont.

Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His
100 105 110

Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln
145 150 155 160

Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp
180 185 190

Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240

Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe
275 280 285

Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala
290 295 300

Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly
325 330 335

Pro Ala Pro Val Glu Ser Leu Gly Gly Glu Glu Glu Ile
340 345

<210> 18
<211> 1047
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

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<222> (1)..(1047)

<400> 18

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Met	Gln	Arg	Leu	Gly	Gly	Ile	Leu	Leu	Cys	Thr	Leu	Leu	Ala	Ala	Ala	
1				5					10					15		
gtc	ccc	act	gct	cct	gct	cct	tcc	ccg	acg	gtc	act	tgg	act	ccg	gcg	96
Val	Pro	Thr	Ala	Pro	Ala	Pro	Ser	Pro	Thr	Val	Thr	Trp	Thr	Pro	Ala	
			20					25					30			
gag	ccg	ggc	cca	gct	ctc	aac	tac	cct	cag	gag	gaa	gct	acg	ctc	aat	144
Glu	Pro	Gly	Pro	Ala	Leu	Asn	Tyr	Pro	Gln	Glu	Glu	Ala	Thr	Leu	Asn	
		35					40					45				
gag	atg	ttt	cga	gag	gtg	gag	gag	ctg	atg	gaa	gac	act	cag	cac	aaa	192
Glu	Met	Phe	Arg	Glu	Val	Glu	Glu	Leu	Met	Glu	Asp	Thr	Gln	His	Lys	
	50					55					60					
ctg	cgc	agt	gcc	gtg	gag	gag	atg	gag	gcg	gaa	gaa	gca	gct	gct	aaa	240
Leu	Arg	Ser	Ala	Val	Glu	Glu	Met	Glu	Ala	Glu	Glu	Ala	Ala	Ala	Lys	
	65				70					75					80	
acg	tcc	tct	gag	gtg	aac	ctg	gca	agc	tta	cct	ccc	aac	tat	cac	aat	288
Thr	Ser	Ser	Glu	Val	Asn	Leu	Ala	Ser	Leu	Pro	Pro	Asn	Tyr	His	Asn	
				85					90					95		
gag	acc	agc	acg	gag	acc	agg	gtg	gga	aat	aac	aca	gtc	cat	gtg	cac	336
Glu	Thr	Ser	Thr	Glu	Thr	Arg	Val	Gly	Asn	Asn	Thr	Val	His	Val	His	
			100					105					110			
cag	gaa	gtt	cac	aag	ata	acc	aac	aac	cag	agt	gga	cag	gtg	gtc	ttt	384
Gln	Glu	Val	His	Lys	Ile	Thr	Asn	Asn	Gln	Ser	Gly	Gln	Val	Val	Phe	
		115					120					125				
tct	gag	aca	gtc	att	aca	tct	gta	ggg	gat	gaa	gaa	ggc	aag	agg	agc	432
Ser	Glu	Thr	Val	Ile	Thr	Ser	Val	Gly	Asp	Glu	Glu	Gly	Lys	Arg	Ser	
	130					135						140				
cat	gaa	tgt	atc	att	gat	gaa	gac	tgt	ggg	ccc	acc	agg	tac	tgc	cag	480
His	Glu	Cys	Ile	Ile	Asp	Glu	Asp	Cys	Gly	Pro	Thr	Arg	Tyr	Cys	Gln	
	145				150					155					160	
ttc	tcc	agc	ttc	aag	tac	acc	tgc	cag	cca	tgc	cgg	gac	cag	cag	atg	528
Phe	Ser	Ser	Phe	Lys	Tyr	Thr	Cys	Gln	Pro	Cys	Arg	Asp	Gln	Gln	Met	
				165					170					175		
cta	tgc	acc	cga	gac	agt	gag	tgc	tgt	gga	gac	cag	ctg	tgt	gcc	tgg	576
Leu	Cys	Thr	Arg	Asp	Ser	Glu	Cys	Cys	Gly	Asp	Gln	Leu	Cys	Ala	Trp	
			180					185					190			
ggt	cac	tgc	acc	caa	aag	gcc	acc	aaa	ggt	ggc	aat	ggg	acc	atc	tgt	624
Gly	His	Cys	Thr	Gln	Lys	Ala	Thr	Lys	Gly	Gly	Asn	Gly	Thr	Ile	Cys	
		195					200					205				

B1
Cont

gac aac cag agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg 210 215 220	672
ggc ctg ctg ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctg Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu 225 230 235 240	720
tgc cat gac ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu 245 250 255	768
gag cct gaa gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu 260 265 270	816
tgc cag cca cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe 275 280 285	864
gtg ggc agc cat gac cac agt gag gag agc cag ctg ccc agg gag gcc Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala 290 295 300	912
ccg gat gag tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu 305 310 315 320	960
ctg gaa gac ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly 325 330 335	1008
cct gcc cct gtg gag tca cta gcc gga gag gag gag att Pro Ala Pro Val Glu Ser Leu Gly Gly Glu Glu Glu Ile 340 345	1047

<210> 19
 <211> 8
 <212> PRT
 <213> synthtic construct

<400> 19
 Asp Tyr Lys Asp Asp Asp Asp Lys
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B1
cont